

# SEQUENCE LISTING

<110> Afar, Daniel E. H.  
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Raitano, Arthur B.  
Saffran, Douglas C.  
Mitchell, Stephen C.  
Jakobovits, Aya  
Faris, Mary  
Vivanco, Igo

<120> NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS  
AND THERAPY OF PROSTATE AND COLON CANCER

<130> 511582000820

<140> 09/615,285

<141> 2000-07-12

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<151> 1999-06-01

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<151> 1999-04-14

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Met Ala  
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ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac cat 165  
Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His  
5 10 15

gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc 213  
 Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro  
 20 25 30

act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc 261  
 Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro  
 35 40 45 50

cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc tgc 309  
 Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys  
 55 60 65

acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act aag 357  
 Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys  
 70 75 80

C1 aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct 405  
 Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala  
 85 90 95

gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc tcc 453  
 Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser  
 100 105 110

aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct 501  
 Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser  
 115 120 125 130

aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag aat 549  
 Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn  
 135 140 145

cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca 597  
 Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser  
 150 155 160

tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac gag 645  
 Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu  
 165 170 175

aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat ttt 693  
 Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe  
 180 185 190

tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt atg 741  
 Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met  
 195 200 205 210

aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg tac 789  
 Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr  
 215 220 225

cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata 837  
 His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile  
 230 235 240

gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc 885

Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly  
245 250 255

ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac 933  
Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His  
260 265 270

gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag tgg 981  
Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp  
275 280 285 290

atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca tgg 1029  
Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp  
295 300 305

cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat 1077  
His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr  
310 315 320

gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat tat gac 1125  
Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp  
325 330 335

tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag cct 1173  
Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro  
340 345 350

ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca ggc 1221  
Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly  
355 360 365 370

atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg gcc 1269  
Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala  
375 380 385

acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag gtg 1317  
Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val  
390 395 400

ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac aac 1365  
Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn  
405 410 415

ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac gtc 1413  
Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val  
420 425 430

gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aag aac 1461  
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn  
435 440 445 450

aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt gcc 1509  
Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala  
455 460 465

aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg gac 1557  
Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp

470

475

480

tgg att tat cga caa atg agg gca gac ggc t aatccacatg gtcttcgtcc 1608  
 Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly  
 485 490

ttgacgtcgt tttaacaagaa aacaatgggg ctggttttgc ttccccgtgc atgatttact 1668  
 cttagagatg attcagaggt cacttcattt ttattaaaca gtgaacttgt ctggcaaaaa 1728  
 aaaaaaaaaa 1738

&lt;210&gt; 2

&lt;211&gt; 492

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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 Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val  
 20 25 30  
 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro  
 35 40 45  
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val  
 50 55 60  
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys  
 65 70 75 80  
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val  
 85 90 95  
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys  
 100 105 110  
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn  
 115 120 125  
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp  
 130 135 140  
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val  
 145 150 155 160  
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp  
 165 170 175  
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn  
 180 185 190  
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser  
 195 200 205  
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys  
 210 215 220  
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg  
 225 230 235 240  
 Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile  
 245 250 255  
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser  
 260 265 270  
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro  
 275 280 285  
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn  
 290 295 300  
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met  
 305 310 315 320  
 Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn

Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln  
 325 340 345 350  
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn  
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 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp  
 370 375 380  
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala  
 385 390 395 400  
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr  
 405 410 415  
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly  
 420 425 430  
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser  
 435 440 445  
 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly  
 450 455 460  
 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe  
 465 470 475 480  
 Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly  
 485 490

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 Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn  
 5 10 15  
  
 cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc 155  
 His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val  
 20 25 30  
  
 ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg 203  
 Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val  
 35 40 45  
  
 ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc 251  
 Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val  
 50 55 60 65  
  
 tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act 299  
 Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr  
 70 75 80  
  
 aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga 347

Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly  
                     85                                    90                                    95

gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc 395  
 Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys  
                     100                                    105                                    110

tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc 443  
 Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro  
                     115                                    120                                    125

tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag 491  
 Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu  
                     130                                    135                                    140                                    145

aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac 539  
 Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met Tyr  
                     150                                    155                                    160

tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac 587  
 Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn  
                     165                                    170                                    175

gag aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat 635  
 Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn  
                     180                                    185                                    190

ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt 683  
 Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe  
                     195                                    200                                    205

atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg 731  
 Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu  
                     210                                    215                                    220                                    225

tac cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt 779  
 Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys  
                     230                                    235                                    240

tta gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg atc gtg 827  
 Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val  
                     245                                    250                                    255

ggc ggt gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg 875  
 Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu  
                     260                                    265                                    270

cac gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag 923  
 His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu  
                     275                                    280                                    285

tgg atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca 971  
 Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro  
                     290                                    295                                    300                                    305

tgg cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc 1019  
 Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe

	310	315	320	
	tat gga gcc gga tac caa gta caa aaa gtg att tct cat cca aat tat			1067
	Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn Tyr			
	325	330	335	
	gac tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag			1115
	Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys			
	340	345	350	
	cct ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca			1163
	Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro			
	355	360	365	
C	ggc atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg			1211
	Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly			
	370	375	380	385
	gcc acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag			1259
	Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys			
	390	395	400	
	gtg ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac			1307
	Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp			
	405	410	415	
	aac ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac			1355
	Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn			
	420	425	430	
	gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aac			1403
	Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Asn			
	435	440	445	
	aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt			1451
	Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys			
	450	455	460	465
	gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg			1499
	Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr			
	470	475	480	
	gac tgg att tat cga caa atg aag gca aac ggc ta atccacatgg			1544
	Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly			
	485	490		
	tcttcgtcct tgacgtcgtt ttacaagaaa acaatggggc tggttttgct tccccgtgca			1604
	tgatttactc ttagagatga ttcagaggtc acttcatttt tattaaacag tgaacttgct			1664
	tggctttggc actctctgcc atactgtgca ggctgcagt gctcccctgc ccagcctgct			1724
	ctccctaacc ccttgccgc aaggggtgat ggccggctgg ttgtgggcac tggcgggtcaa			1784
	ttgtggaagg aagaggggtg gaggtgccc ccattgagat cttcctgctg agtcctttcc			1844
	aggggccaat tttggatgag catggagctg tcacttctca gctgctggat gacttgagat			1904
	gaaaaaggag agacatggaa agggagacag ccaggtggca cctgcagcgg ctgccctctg			1964
	gggccacttg gtagtgctcc cagcctactt cacaagggga ttttgctgat gggttcttag			2024
	agccttagca gccctggatg gtggccagaa ataaaggac cagcccttca tgggtggtga			2084
	cgtggtagtc acttgtaagg ggaacagaaa catttttgtt cttatggggg gagaatatag			2144
	acagtgccct tgggtgcgagg gaagcaattg aaaaggaact tgccctgagc actcctggtg			2204

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 cgccaagttt ggcacatgt cggcctcttc aggectgata gtcattggaa attgaggtcc 2384  
 atgggggaaa tcaaggatgc tcagtttaag gtacactgtt tccatgttat gtttctacac 2444  
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 <211> 492  
 <212> PRT  
 <213> Homo sapiens

<400> 4

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 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro  
 35 40 45  
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val  
 50 55 60  
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys  
 65 70 75 80  
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val  
 85 90 95  
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys  
 100 105 110  
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn  
 115 120 125  
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp  
 130 135 140  
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met  
 145 150 155 160  
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp  
 165 170 175  
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn  
 180 185 190  
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser  
 195 200 205  
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys  
 210 215 220  
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg  
 225 230 235 240  
 Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile  
 245 250 255  
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser  
 260 265 270  
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro  
 275 280 285  
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn  
 290 295 300  
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met  
 305 310 315 320  
 Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn  
 325 330 335  
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln  
 340 345 350  
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn



355                      360                      365  
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp  
 370                      375                      380  
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala  
 385                      390                      395                      400  
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr  
 405                      410                      415  
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly  
 420                      425                      430  
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser  
 435                      440                      445  
 Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly  
 450                      455                      460  
 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe  
 465                      470                      475                      480  
 Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly  
 485                      490

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 <212> DNA  
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<220>  
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 <222> (1)...(388)  
 <223> n = A,T,C or G

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 gcacctgcag cggtgcccct ctggggccac ttggtagtgt ccccgacctt cctctccaca 180  
 aggggatttt gctgatgggt tcttanagcc ttagcagccc tggatgggtg ccagaaataa 240  
 agggaccagc ccttcattgg tggtgacgtg gtantcactt gtaaggggaa cagaaacatt 300  
 tttgttctta tggggtgaga atatagacag tgcccttggt gcgaggggaa caattgaaaa 360  
 ggaacttgcc ctgagcactc ctggtgca 388

<210> 6  
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 <212> DNA  
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<400> 7

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<210> 9  
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<212> DNA  
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<400> 9  
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<210> 10  
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<212> DNA  
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<223> Nester PCR Primer (NP) 1

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<210> 11  
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<223> Nester PCR Primer (NP) 2

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<220>  
<223> RT-PCR Primer 1A

<400> 12  
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<210> 13  
<211> 25  
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<220>  
<223> RT-PCR Primer 1B

<400> 13  
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25

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